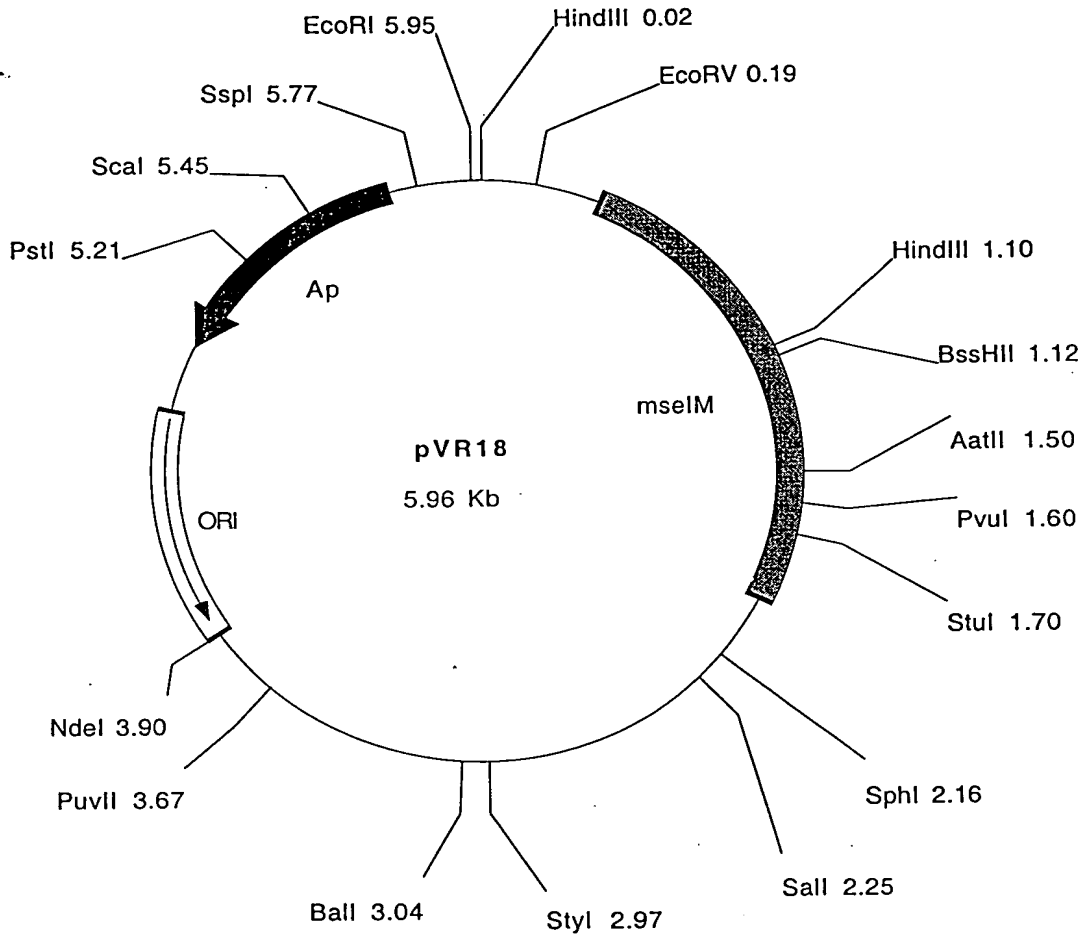
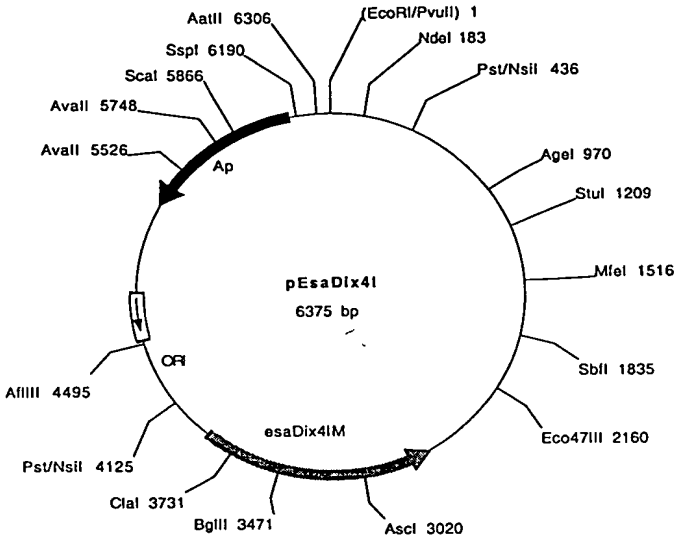


Fig. 1

A.



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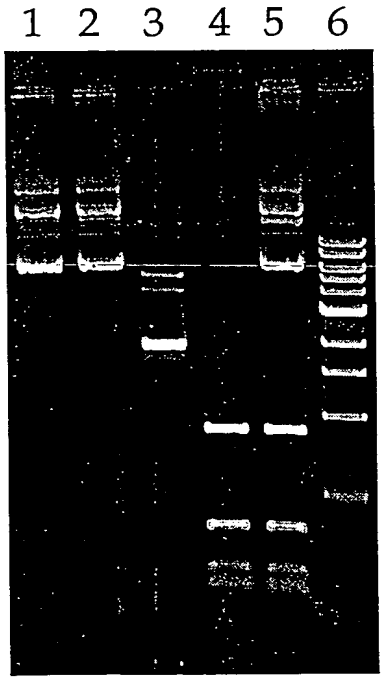

Fig 2

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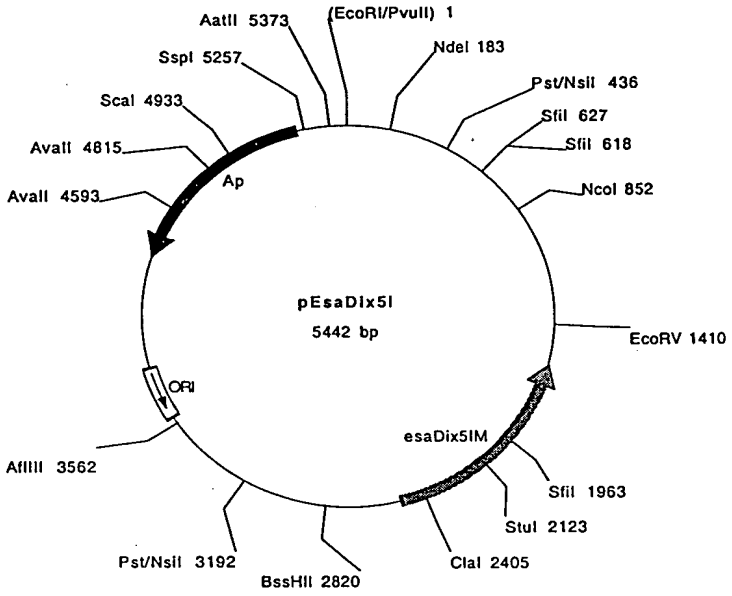

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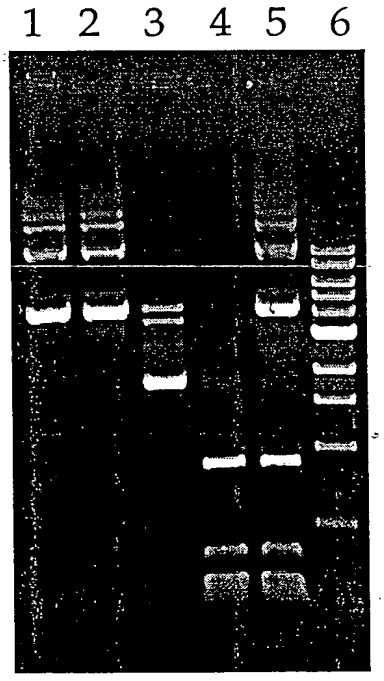

Fig. 3.

NME1 M

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SEQ. ID NO2

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    V  E  A  D  N  L  D  F  I  Q  T  L  P  D  A
 91 AGCTTCCGAATGATCTACATCGATCCGCCGTTCAACACAGGGCGA
    S  F  R  M  I  Y  I  D  P  P  F  N  T  G  R
136 ACGCAGCGGCTTCAGTCGCTCAAGACGACCCGCTCGGTCACAGGG
    T  Q  R  L  Q  S  L  K  T  T  R  S  V  T  G
181 TCGCGAGTCGGCTTCAAAGGCCAGACGTACGACACGGTCAAGAGC
    S  R  V  G  F  K  G  Q  T  Y  D  T  V  K  S
226 ACTCTGCACTCGTATGACGACGCTTTCACCGACTATTGGTCGTTC
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271 CTCGAACCGCGTCTCCTGGAGGCTTGGCGGTTGCTCACCCCTGAC
    L  E  P  R  L  L  E  A  W  R  L  L  T  P  D
316 GGCGCGCTCTATCTTCATCTGGATTACCGCGAGGTTCACTACGCC
    G  A  L  Y  L  H  L  D  Y  R  E  V  H  Y  A
361 AAGGTCGTCCTCGACGCGATGTTCGGACGCGAAAGCTTCCTGAAC
    K  V  V  L  D  A  M  F  G  R  E  S  F  L  N
406 GAGCTGATCTGGGCGTACGACTACGGCGCGCGCTCGAAGAGCAAG
    E  L  I  W  A  Y  D  Y  G  A  R  S  K  S  K
451 TGGCCCACCAAGCACGACAACATCCTCGTGTATGTGAAGGACCCG
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496 AACAACTACGTCTGGAACGGTCAGGATGTAGATCGCGAGCCCTAC
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    K  E  R  T  G  Y  A  T  Q  K  P  V  G  I  I
676 CGTCGCATGATTCAGGCGAGCAGCAATGAAGGCGACTGGGTTCTG
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721 GATTTCTTCGCTGGTAGTGGGACGACCGGCGCCGCGGCCCGCCAG
    D  F  F  A  G  S  G  T  T  G  A  A  A  R  Q
766 CTCGGACGCCGTTTTGTGCTCGTAGACGTCAACCCAGAAGCAATC
    L  G  R  R  F  V  L  V  D  V  N  P  E  A  I
811 GCGGTAATGGCAAAACGGTTGGATGACGGGGCATTGGACACCAGC
    A  V  M  A  K  R  L  D  D  G  A  L  D  T  S
856 GTGACGATCGTGCAGACTCCCCAGAGTGACCCACGAACCGACGGA
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Fig. 4.

esqDix 4IM

SEQ ID NO 3
SEQ ID NO 4

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  91 TCACCGCCTAATCGTCTGATTTGGGCGGACAACCTGCCGCTAATG
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 136 GTAGATTTGTTGGCCGAATATGAAGGGAAAATCGATCTGATCTAC
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 181 GCCGATCCCCCTTTTTTTACGGATCGTACTTATGCGGCGCGAATT
     A  D  P  P  F  F  T  D  R  T  Y  A  A  R  I
 226 GGTCATGGGGAGGATTCGCGTCGTCCACAAACCTGGCAGCTTGCA
     G  H  G  E  D  S  R  R  P  Q  T  W  Q  L  A
 271 GAAGGATATACGGACGAGTGGAAGGATTTAGATGAATACCTGGAC
     E  G  Y  T  D  E  W  K  D  L  D  E  Y  L  D
 316 TTCCTTTATCCACGCCTGGTACTGATGTATCGACTGCTGGCACCA
     F  L  Y  P  R  L  V  L  M  Y  R  L  L  A  P
 361 CACGGAACGCTCTACTTGCACCTGGACTGGCACGCCAATGCCTAC
     H  G  T  L  Y  L  H  L  D  W  H  A  N  A  Y
 406 GTACGTGTACTGCTTGATGAGATCTTCGGGCGACAGCGGTTTCTC
     V  R  V  L  L  D  E  I  F  G  R  Q  R  F  L
 451 AACGAGATCGTCTGGATCTATCACGGCCCCTCAGCCATCCGACGC
     N  E  I  V  W  I  Y  H  G  P  S  A  I  R  R
 496 GCCTTCAAGCGCAAACATGATACCATCTTGGTTTATGTGAAAGGT
     A  F  K  R  K  H  D  T  I  L  V  Y  V  K  G
 541 GAAAACTATACATTCAATGCGGATGCGGTTCGTCAACCTTACCAT
     E  N  Y  T  F  N  A  D  A  V  R  Q  P  Y  H
 586 CCGAGCACNCATAAGACCTTCGCTTCCTCCCCGAAGGCCGGCTTT
     P  S  T  H  K  T  F  A  S  S  P  K  A  G  F
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     G  K  V  P  D  L  Q  R  G  K  V  P  E  D  W
 676 TGGTATTTTCCGGTCGTGGCCCGTCTACACCGAGAACGGAGCGGC
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 766 GCCTCCTCGAACGCAGGCGATCTGGTGGCAGACTTCTTCTGCGGC
     A  S  S  N  A  G  D  L  V  A  D  F  F  C  G
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     L  V  N  D  A  S  W  R  A  V  H  V  T  R  T
 901 CGCTTGCTACGCGAGGGAGTAAGTTTCACTTTTGAACGCCAGGAA
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 946 ACTTTTACTCTACCTATCCAGCCACTTCCACCAGATTGGTTGATC
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 991 ATCGCCGAGGAGCAGATTCGCCTCCAAGCACCCTTTCTCGTAGAT
     I  A  E  E  Q  I  R  L  Q  A  P  F  L  V  D
1036 TTTTGGGAAGTGGACGATCAATGGGATGGCAAAATCTTCCGCAGC
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1081 CGTCATCAAGGCTTACGCTCCCGCCTTCAGGAGCAGGCGCCGCTC
     R  H  Q  G  L  R  S  R  L  Q  E  Q  A  P  L
1126 TCTCTACCATTGACCGGGAATGGACTGTTGTGTGTACGGGTAGTG
     S  L  P  L  T  G  N  G  L  L  C  V  R  V  V
1171 AGCCGTGAAGGGGAATACTATGAGTTCACAGGTCGAGCCGATAGC
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     P  H  P  V  S  F  *
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Fig. 5

esa DixSIM

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SEQ ID:6

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91 GTGGACCTGATCTACATCGATCCTCCGTTCAACACCGGAAAGGTT
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136 CAGGAGCGCACTCAGCTCAAAACGGTGCGCTCCGAGTGGGGCGAT
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181 CGCGTCGGATTCCAGGGCCGTCGCTACGAAAGCATCGTCGTGGGT
   R  V  G  F  Q  G  R  R  Y  E  S  I  V  V  G
226 AAGAAGCGCTTTACCGACTTCTTCGACGACTATCTGGCTTTCCTG
   K  K  R  F  T  D  F  F  D  D  Y  L  A  F  L
271 GAACCGCGCCTGGTCGAAGCCCATCGTGTTCTGGCGCCGCACGGG
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316 TGCCTCTACTTTCACGTCGACTACCGCGAGGTGCACTACTGTAAG
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361 GTCCTTCTTGACGGCATCTTCGGTCGCGAGGCCTTTCTCAACGAG
   V  L  L  D  G  I  F  G  R  E  A  F  L  N  E
406 ATCATCTGGGCCTACGATTACGGCGGGCGTCCGAAGGACAGGTGG
   I  I  W  A  Y  D  Y  G  G  R  P  K  D  R  W
451 CCTCCTAAGCACGACAACATCCTGCTCTACGCCAAGACTCCCGGT
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496 CGCCACGTGTTCAATGCGGACGAAATCGAGCGCATTCCCTACATG
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541 GCTCCGGGCCTGGTTGGCCCCGAAAAGGCAGCCCGTGGAAAACTG
   A  P  G  L  V  G  P  E  K  A  A  R  G  K  L
586 CCAACCGACACGTGGTGGCATACGATCGTTCCGACCAGCGGCTCC
   P  T  D  T  W  W  H  T  I  V  P  T  S  G  S
631 GAGAAGACCGGGTATCCAACCCAGAAACCTTTAGGGATTCTCCGC
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676 CGTATTGTGCAGGCATCGTCTCATCCGGGGGCAGTCGTGCTCGAC
   R  I  V  Q  A  S  S  H  P  G  A  V  V  L  D
721 TTCTTCGCCGGCAGTGGGACAACAGGGGTAGCGGCTTTTGAGTTG
   F  F  A  G  S  G  T  T  G  V  A  A  F  E  L
766 GGCCGGCGTTTCATTCTGGTCGATAACCATCCGGAGGCCCTCCAG
   G  R  R  F  I  L  V  D  N  H  P  E  A  L  Q
811 GTGATGGCCAGGCGCTTCGACGGCATCGAGGGGATCGAATGGGTG
   V  M  A  R  R  F  D  G  I  E  G  I  E  W  V
856 GGCTTCGATCCGACACCGTACCAGAAGGGCGCAAAGCAGCGCCGC
   G  F  D  P  T  P  Y  Q  K  G  A  K  Q  R  R
901 TCCTGCCCGGCGCCCACCGGGTAA 924
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Fig. 6

mc1R

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 91 GACCCCTGGGTCGGCAGCCCGTTCGAGTGGATCCTTCGCGTTCCA
    D  P  W  V  G  S  P  F  E  W  I  L  R  V  P
136 TCCAGAACGAAGGGCGCGGTCGGTGAGCTGCTCGTGAGCGAATGG
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181 GCTAATGCCAAAGGCCTCCGTGTGAAGAGGTCGGGGTCCAGCGAT
    A  N  A  K  G  L  R  V  K  R  S  G  S  S  D
226 GCGGACCGCGTGATCAACGGGCATCGCATCGAGATCAAGATGTCG
    A  D  R  V  I  N  G  H  R  I  E  I  K  M  S
271 ACTTTGTGGAAGTCCGGCGGCTTCAAGTTTCAGCAGATCCGGGAT
    T  L  W  K  S  G  G  F  K  F  Q  Q  I  R  D
316 CAGGAGTACGACTTTTGCCTCTGCCTTGGGATCAGCCCGTTCGAA
    Q  E  Y  D  F  C  L  C  L  G  I  S  P  F  E
361 GTGCACGCGTGGCTGCTGCCCAAAGACCTATTGCTTGAGTACGTG
    V  H  A  W  L  L  P  K  D  L  L  L  E  Y  V
406 ATTGGTCACATGGGTCAGCACACCGGCGCGAGCGGGAGCGACACT
    I  G  H  M  G  Q  H  T  G  A  S  G  S  D  T
451 GCGTGGCTGGGGTTCCCAGCGGACGAGCCGTATGACTGGATGCGC
    A  W  L  G  F  P  A  D  E  P  Y  D  W  M  R
496 CCTTTCGGAGGTCGCTTAGGTCACGTCGAAGATCTCCTCCTCGCG
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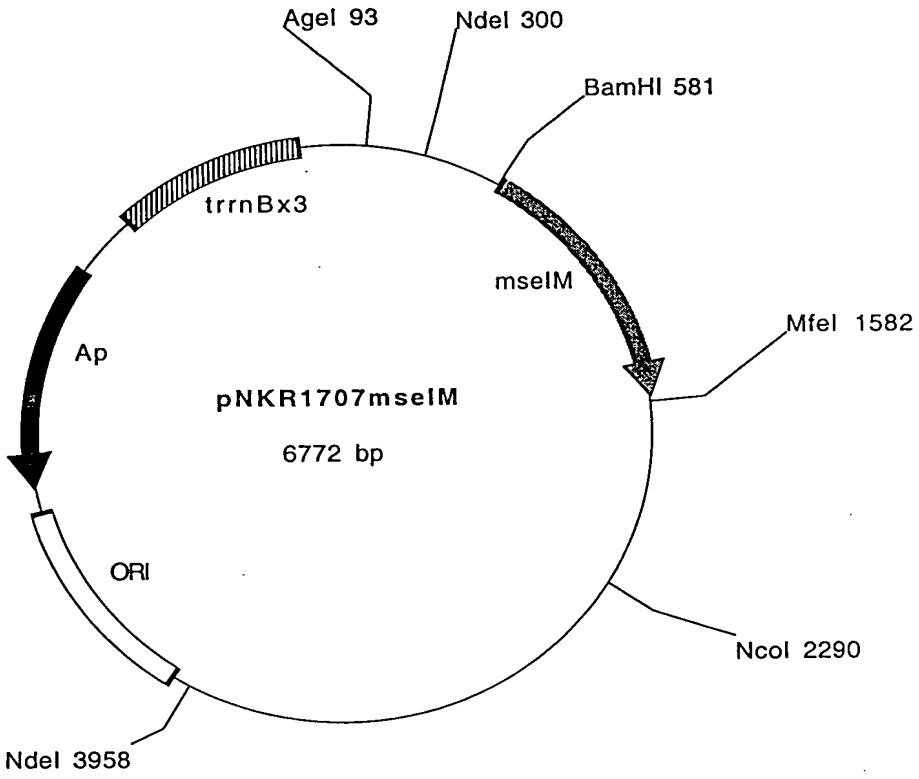
SEQ ID 7
SEQ ID 8

Fig. 7.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ORI
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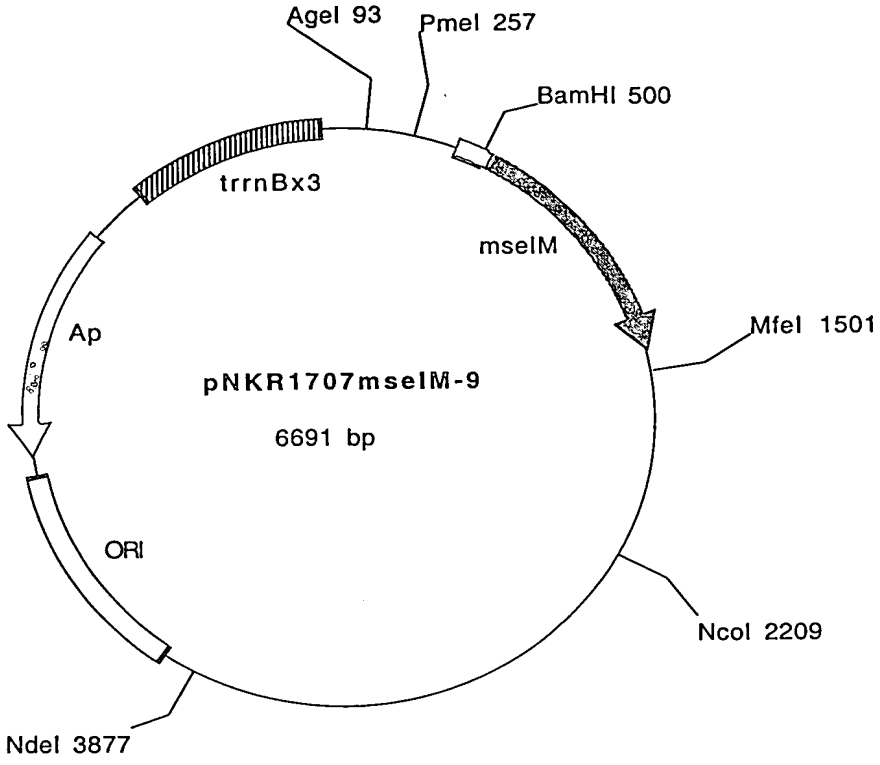
NdeI 3958

Fig. 8.

A.



B.

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*Pme*I
TTGCCCGGTTTTTTTTGCGTTGAATTTGTCATTTTGTGCCGTGGTGTTTAAACCGCAC
-35 -10
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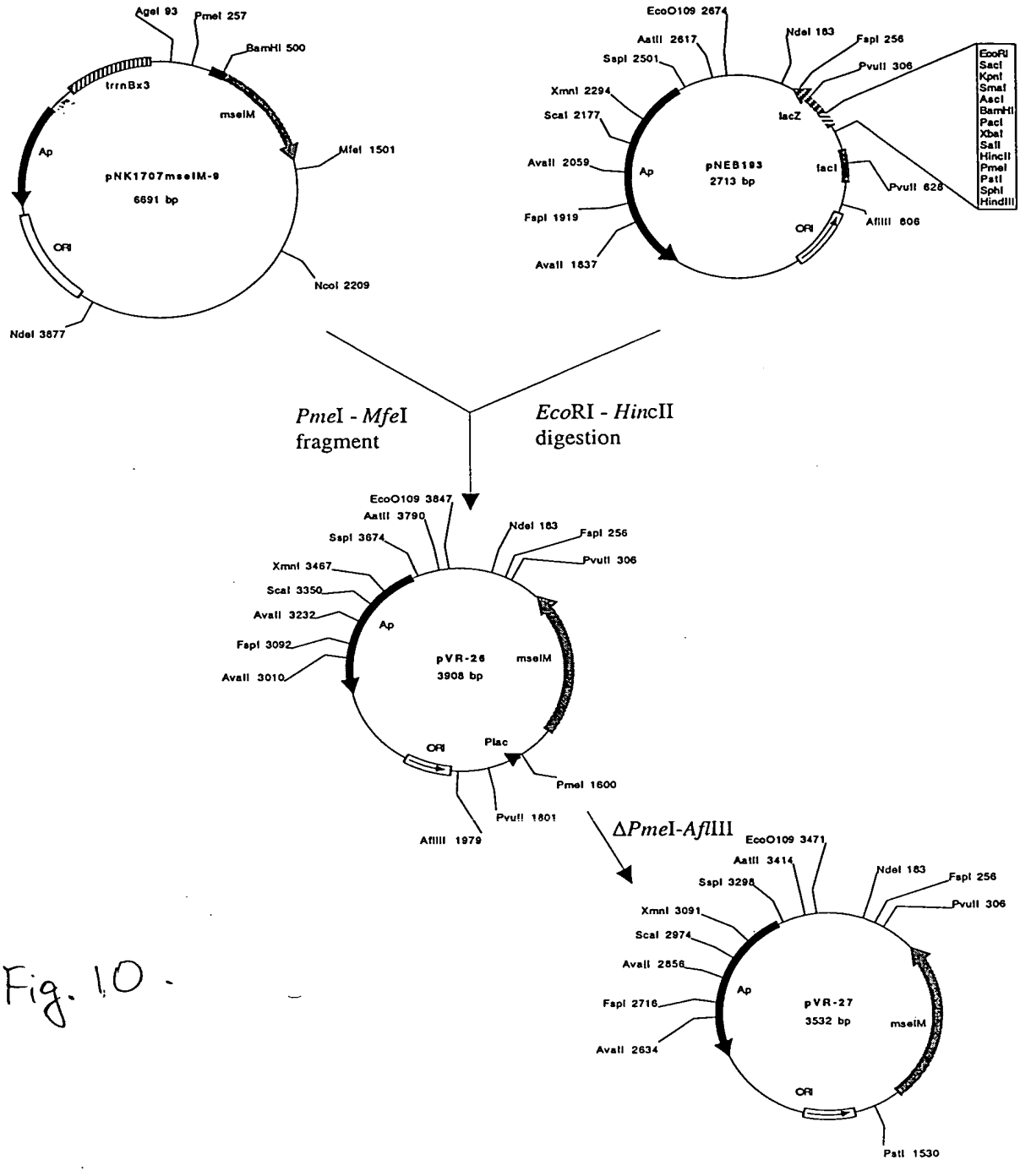
TGGATCC

SEQ ID NO

Fig. 9.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NcoI 2209
NdeI 3877
EcoO109 2674
AatII 2617
NdeI 183
FspI 256
SspI 2501
PvuII 306
XmnI 2294
ScaI 2177
lacZ
AvaII 2059
Ap
pNEB193
2713 bp
lacI
PvuII 628
FspI 1919
AflIII 806
ORI
AvaII 1837
EcoRI
SacI
KpnI
SmaI
AscI
BamHI
PacI
XbaI
SalI
HincII
PmeI
PstI
SphI
HindIII
PmeI - MfeI fragment
EcoRI - HincII digestion
EcoO109 3847
AatII 3790
NdeI 183
FspI 256
SspI 3674
PvuII 306
XmnI 3467
ScaI 3350
AvaII 3232
Ap
FspI 3092
pVR-26
3908 bp
mseIM
AvaII 3010
ORI
Plac
PmeI 1600
PvuII 1601
AflIII 1979
ΔPmeI-AflIII
EcoO109 3471
AatII 3414
NdeI 183
FspI 256
SspI 3298
PvuII 306
XmnI 3091
ScaI 2974
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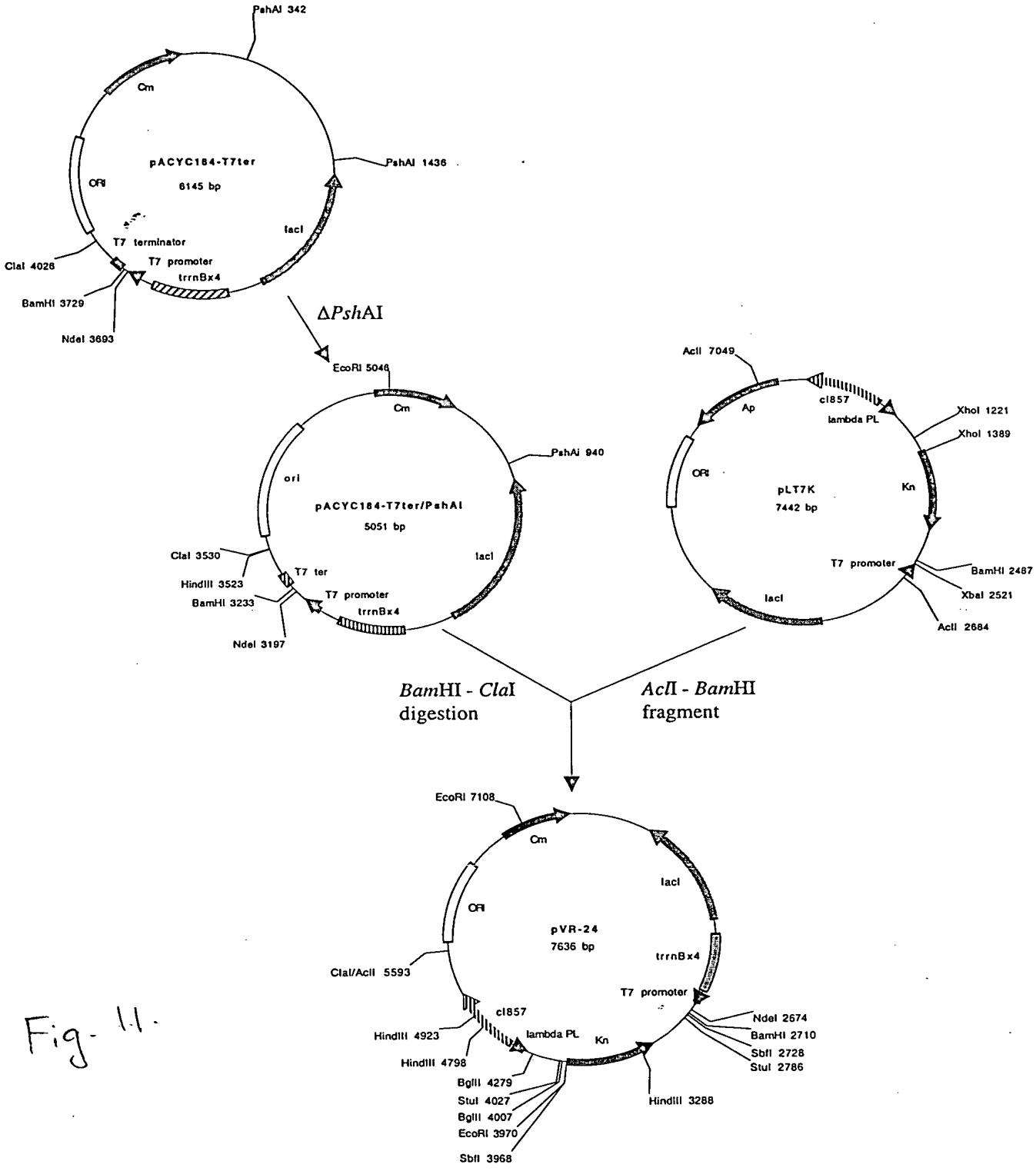
AvaII 2634
ORI
PstI 1530

Fig. 10.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ORI
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lacI
T7 terminator
T7 promoter
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ClaI 4026
BamHI 3729
NdeI 3693
ΔPshAI
EcoRI 5046
Cm
PshAi 940
ori
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lacI
ClaI 3530
T7 ter
HindIII 3523
T7 promoter
BamHI 3233
trrnBx4
NdeI 3197
AclI 7049
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lambda PL
XhoI 1221
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XbaI 2521
lacI
AclI 2684
BamHI - ClaI
digestion
AclI - BamHI
fragment
EcoRI 7108
Cm
lacI
ORI
pVR-24
7636 bp
trrnBx4
ClaI/AclI 5593
T7 promoter
cI857
NdeI 2674
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SbfI 2728
StuI 2786
HindIII 4923
lambda PL
Kn
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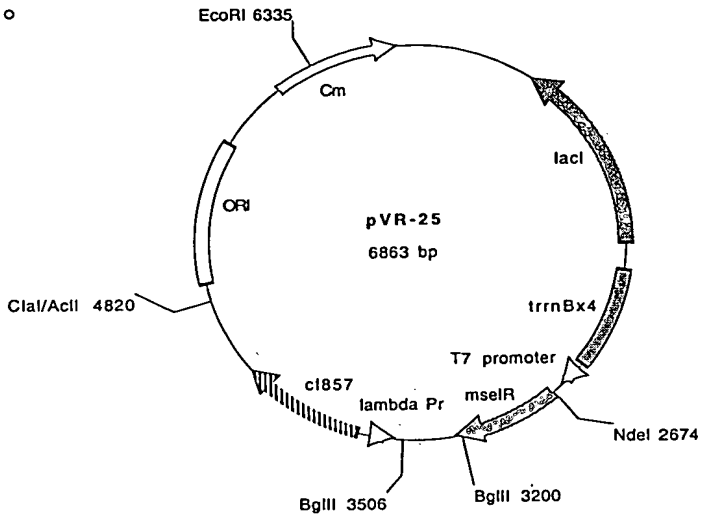
SbfI 3968
HindIII 3288

Fig. 11.

A.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pVR-25
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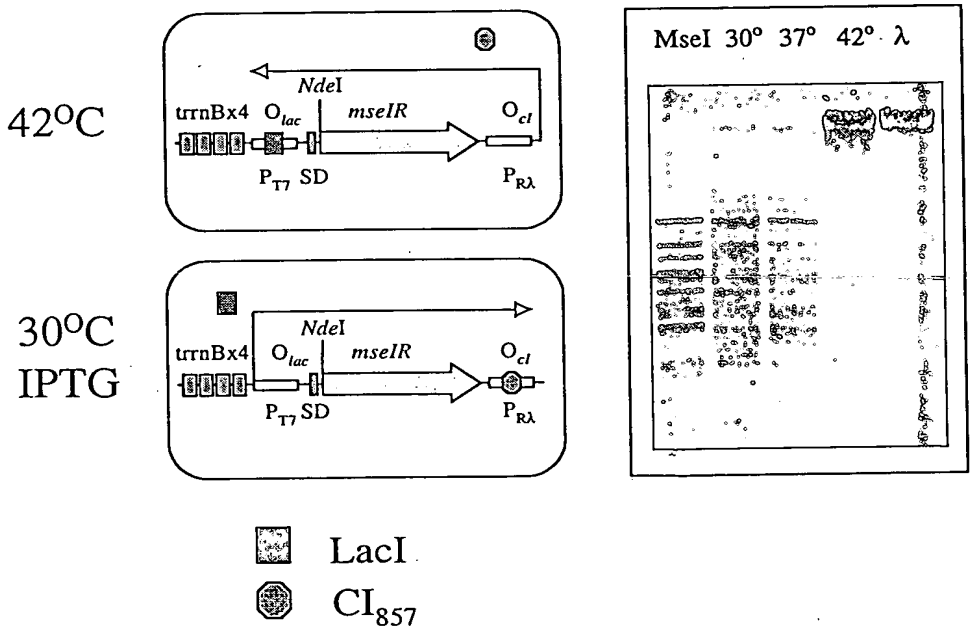
B.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O_{cI}
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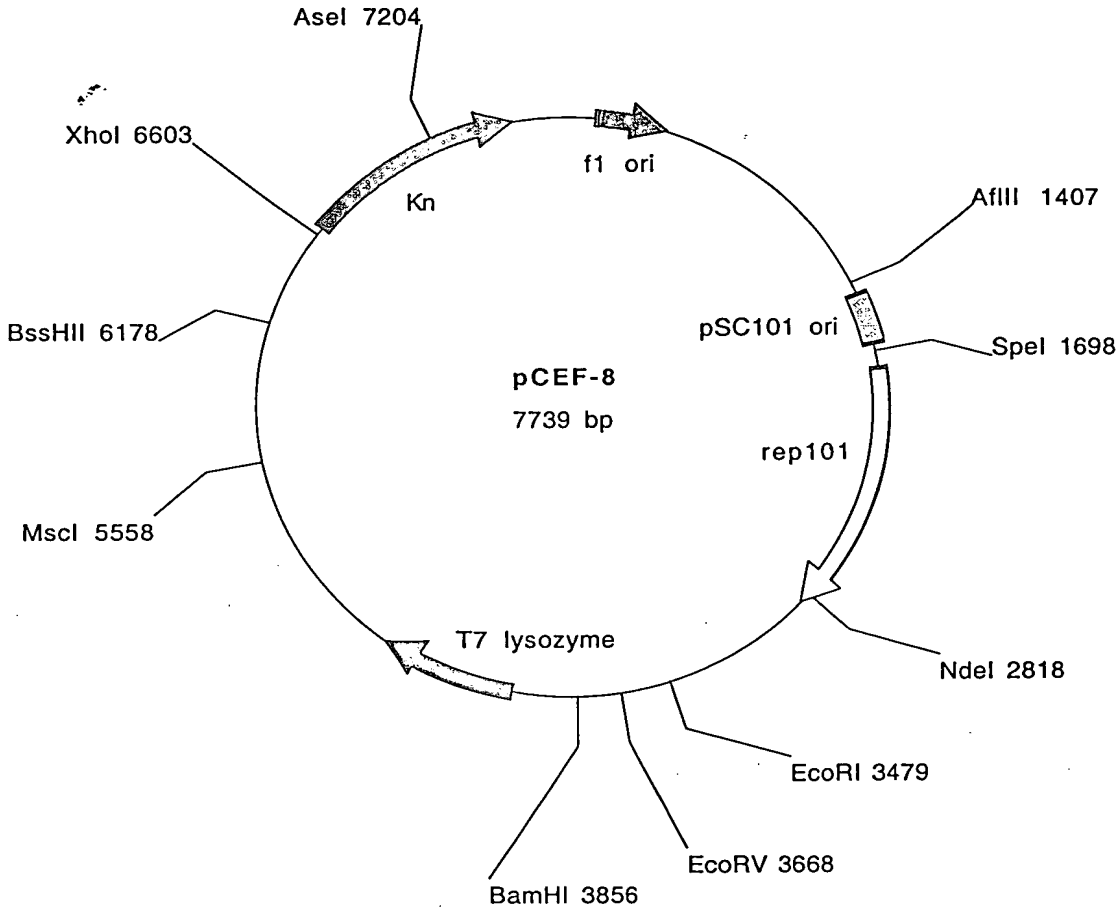
30°C
IPTG
NdeI
trrnBx4
O_{lac}
mseIR
O_{cI}
P_{T7} SD
$P_{R\lambda}$
MseI 30° 37° 42° λ
LacI
CI_{857}

Fig. 12.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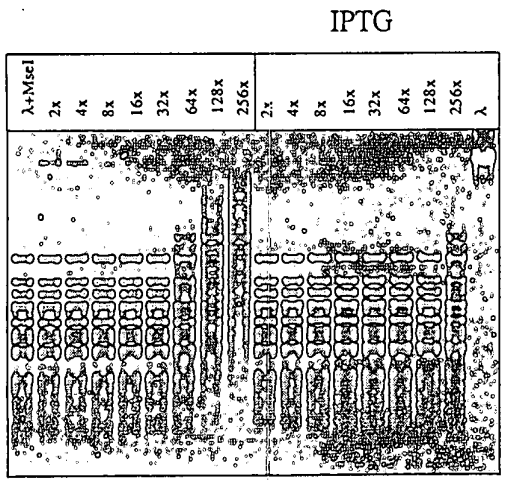
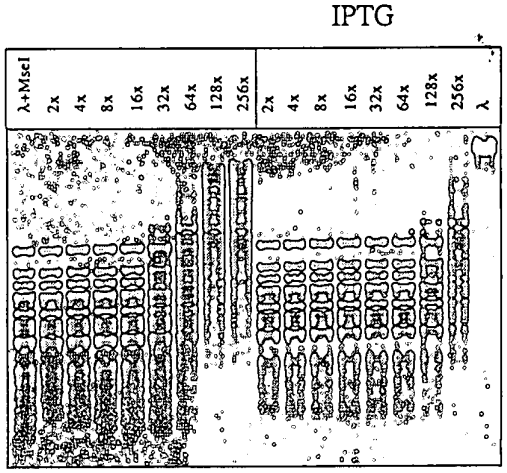
XhoI 6603
f1 ori
Kn
AflII 1407
BssHII 6178
pSC101 ori
SpeI 1698
pCEF-8
7739 bp
rep101
MscI 5558
T7 lysozyme
NdeI 2818
EcoRI 3479
EcoRV 3668
BamHI 3856

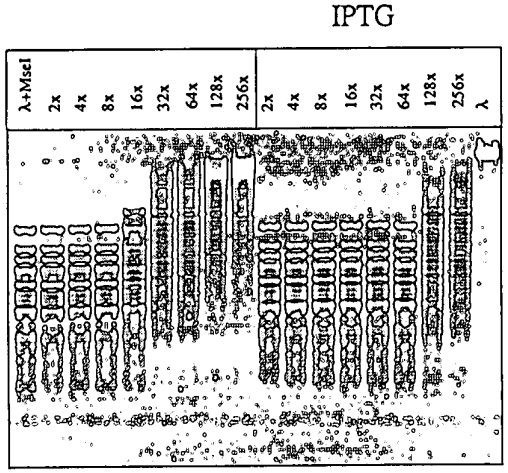
Fig. 13.



MseRM4



MseRM5



MseRM6

Fig. 14

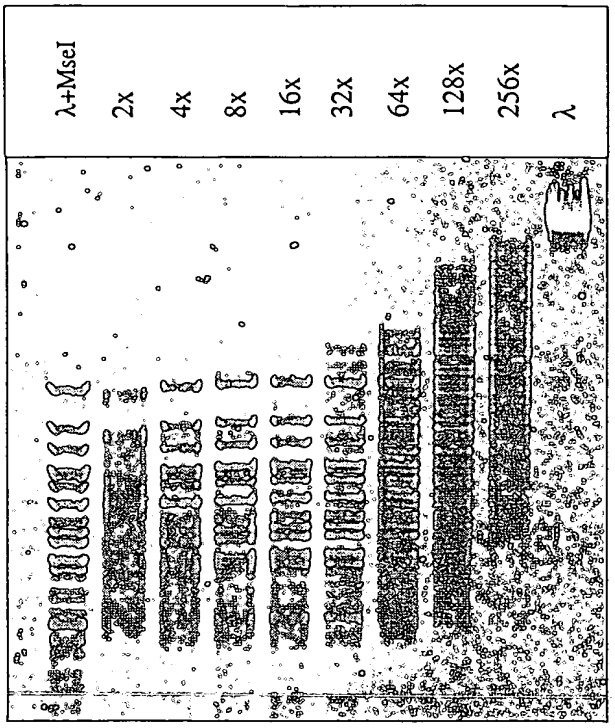


Fig. 15.